```
ATGACCGCTATGAGCACTGCAATTACACGCCAGATCGTTCTCGATACCGAAACCACCGGTATGAACCAGATTGGT  75
                                  mutD
M  T  A  M  S  T  A  I  T  R  Q  I  V  L  D  T  E  T  T  G  M  N  Q  I  G

GCGCACTATGAAGGCCACAAGATCATTGAGATTGGTGCCGTTGAAGTGGTGAACCGTCGCCTGACGGGCAATAAC  150
                                  mutD
A  H  Y  E  G  H  K  I  I  E  I  G  A  V  E  V  V  N  R  R  L  T  G  N  N

TTCCATGTTTATCTCAAACCCGATCGGCTGGTGGATCCGGAAGCCTTTGGCGTACATGGTATTGCCGATGAATTT  225
                                  mutD
F  H  V  Y  L  K  P  D  R  L  V  D  P  E  A  F  G  V  H  G  I  A  D  E  F

TTGCTCGATAAGCCCACGTTTGCCGAAGTAGCCGATGAGTTCATGGACTATATTCGCGGCGCGGAGTTGGTGATC  300
                                  mutD
L  L  D  K  P  T  F  A  E  V  A  D  E  F  M  D  Y  I  R  G  A  E  L  V  I

CATAACGCAGCGTTCGATATCGGCTTTATGGACTACGAGTTTTCGTTGCTTAAGCGCGATATTCCGAAGACCAAT  375
                                  mutD
H  N  A  A  F  D  I  G  F  M  D  Y  E  F  S  L  L  K  R  D  I  P  K  T  N
```

FIG._1A

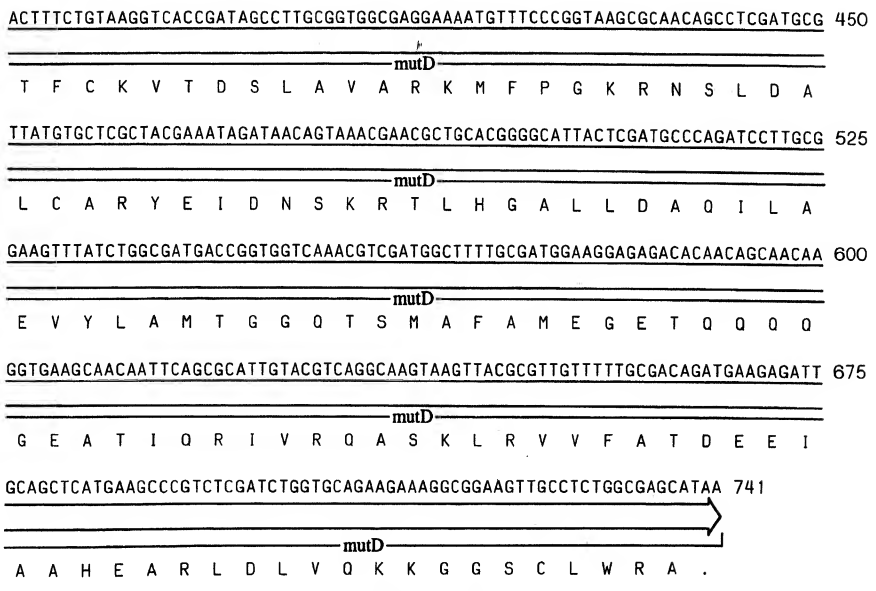

ACTTTCTGTAAGGTCACCGATAGCCTTGCGGTGGCGAGGAAAATGTTTCCCGGTAAGCGCAACAGCCTCGATGCG 450
mutD
T F C K V T D S L A V A R K M F P G K R N S L D A
TTATGTGCTCGCTACGAAATAGATAACAGTAAACGAACGCTGCACGGGGCATTACTCGATGCCCAGATCCTTGCG 525
mutD
L C A R Y E I D N S K R T L H G A L L D A Q I L A
GAAGTTTATCTGGCGATGACCGGTGGTCAAACGTCGATGGCTTTTGCGATGGAAGGAGAGACACAACAGCAACAA 600
mutD
E V Y L A M T G G Q T S M A F A M E G E T Q Q Q Q
GGTGAAGCAACAATTCAGCGCATTGTACGTCAGGCAAGTAAGTTACGCGTTGTTTTTGCGACAGATGAAGAGATT 675
mutD
G E A T I Q R I V R Q A S K L R V V F A T D E E I
GCAGCTCATGAAGCCCGTCTCGATCTGGTGCAGAAGAAAGGCGGAAGTTGCCTCTGGCGAGCATAA 741
mutD
A A H E A R L D L V Q K K G G S C L W R A .

FIG._1B

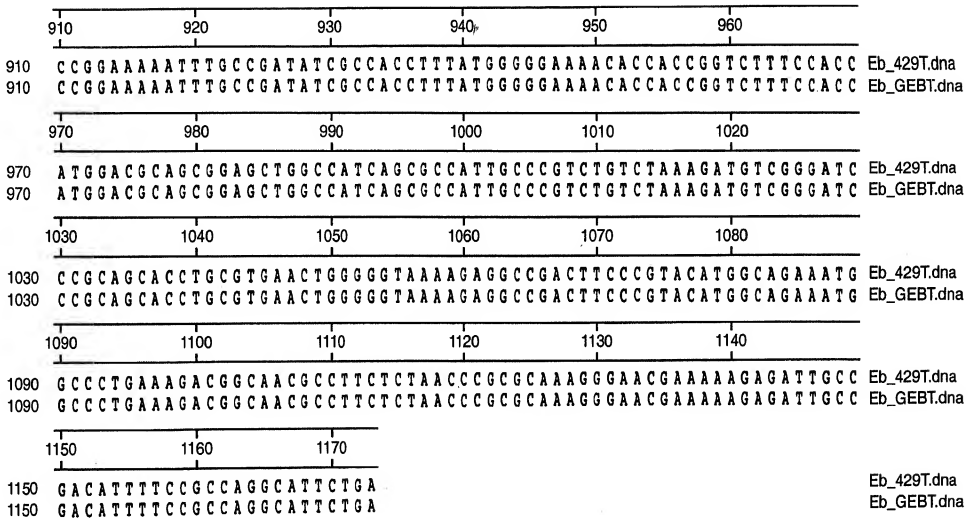
Start	Sequence	Name
10	ATGAGCTATCGTATGTTTGATTATCTGGTTCCAAATGTGAACTTCTTTGGCCCGGGCGCC	Eb_429T.dna
10	ATGAGCTATCGTATGTTTGATTATCTGGTTCCAAATGTRAACTTCTTTGGCCCGGGCGCC	Eb_GEBT.dna
70	GTTTCTGTTGTTGGCCAGCGCTGCCAGCTGCTGGGGGGTAAAAAAGCCCTGCTGGTGACC	Eb_429T.dna
70	GTTTCTGTTGTTGGCCAGCGCTGCCAGCTGCTGGGGGGTAAAAAAGCCCTGCTGGTGACC	Eb_GEBT.dna
130	GATAAGGGCCTGCGCGCCATTAAAGACGGTGCTGTCGATCAGACCGTGAAGCACCTGAAA	Eb_429T.dna
130	GATAAGGGCCTGCGCGCCATTAAAGACGGTGCTGTCGATCAGACCGTGAAGCACCTGAAA	Eb_GEBT.dna
190	GCCGCCGGTATTGAGGTGGTCATTTTCGACGGGGTCGAGCCGAACCCGAAAGACACCAAC	Eb_429T.dna
190	GCCGCCGGTATTGAGGTGGTCATTTTCGACGGGGTCGAGCCGAACCCGAAAGACACCAAC	Eb_GEBT.dna
250	GTGCTCGACGGCCTGGCCATGTTCCGTAAAGAGCAGTGCGACATGATAATCACCGTCGGC	Eb_429T.dna
250	GTGCTCGACGGCCTGGCCATGTTCCGTAAAGAGCAGTGCGACATGATAATCACCGTCGGC	Eb_GEBT.dna

FIG._2A

FIG._2B

```
     610       620       630       640       650       660
610  ACCCACGCGGTAGAGGCCTATATCTCCAAAGACGCCAACCCGGTTACCGATGCCTCTGCT  Eb_429T.dna
610  ACCCACGCGGTAGAGGCCTATATCTCCAAAGACGCCAACCCGGTTACCGATGCCTCTGCT  Eb_GEBT.dna

     670       680       690       700       710       720
670  ATTCAGGCCATCAAACTGATTGCCACCAACTTGCGCCAGGCCGTCGCCCTGGGGACCAAC  Eb_429T.dna
670  ATTCAGGCCATCAAACTGATTGCCACCAACTTGCGCCAGGCCGTCGCCCTGGGGACCAAC  Eb_GEBT.dna

     730       740       750       760       770       780
730  CTCAAAGCCCGTGAAAACATGGCCTGCGCCTCTCTGCTGGCCGGGATGGCCTTTAACAAC  Eb_429T.dna
730  CTCAAAGCCCGTGAAAACATGGCCTGCGCCTCTCTGCTGGCCGGGATGGCCTTTAACAAC  Eb_GEBT.dna

     790       800       810       820       830       840
790  GCCAACCTGGGCTATGTTCACGCCATGGCTCACCAGCTGGGCGGCCTGTACGACATGGCC  Eb_429T.dna
790  GCCAACCTGGGCTATGTTCACGCCATGGCTCACCAGCTGGGCGGCCTGTACGACATGGCC  Eb_GEBT.dna

     850       860       870       880       890       900
850  CACGGGGTGGCGAACGCGGTCCTGCTGCCCCATGTCTGCCGCTATAACCTGATTGCCAAC  Eb_429T.dna
850  CACGGGGTGGCGAACGCGGTCCTGCTGCCCCATGTCTGCCGCTATAACCTGATTGCCAAC  Eb_GEBT.dna
```

FIG._2C

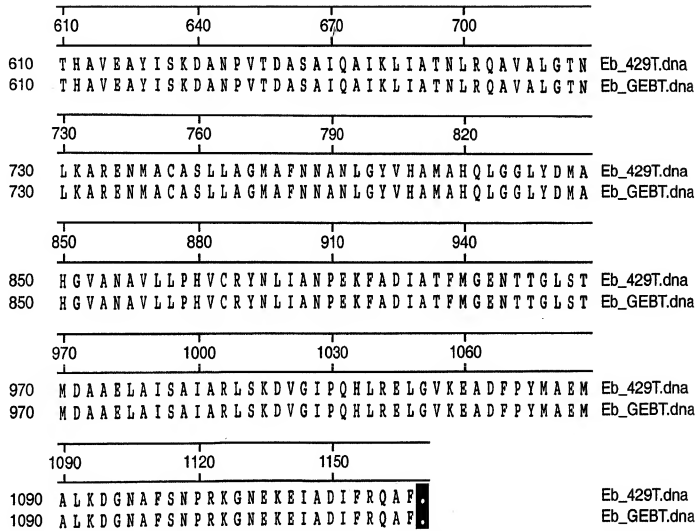


Decoration 'Decoration #1': Shade (with solid black) residues that differ from the Consensus.

FIG._2D

10 40 70 100
10 MSYRMFDYLVPNVNFFGPGAVSVVGQRCQLLGGKKALLVT Eb_429T.dna
10 MSYRMFDYLVPNVNFFGPGAVSVVGQRCQLLGGKKALLVT Eb_GEBT.dna
130 160 190 220
130 DKGLRAIKDGAVDQTVKHLKAAGIEVVIFDGVEPNPKDTN Eb_429T.dna
130 DKGLRAIKDGAVDQTVKHLKAAGIEVVIFDGVEPNPKDTN Eb_GEBT.dna
250 280 310 340
250 VLDGLAMFRKEQCDMITTVGGGSPHDCGKGIGIAATHPGD Eb_429T.dna
250 VLDGLAMFRKEQCDMITTVGGGSPLDCGKGIGIAATHPGD Eb_GEBT.dna
370 400 430 460
370 LYSYAGIETLTNPLPPIIAVNTTAGTASEVTRHCVLTNTK Eb_429T.dna
370 LYSYAGIETLTNPLPPIIAVNTTAGTASEVTRHCVLTNTK Eb_GEBT.dna
490 520 550 580
490 TKVKFVIVSWRNLPSVSINDPLLMIGKPAGLTAATGMDAL Eb_429T.dna
490 TKVKFVIVSWRNLPSVSINDPLLMIGKPAGLTAATGMDAL Eb_GEBT.dna

FIG._3A



Decoration 'Decoration #1': Shade (with solid black) residues that differ from the Consensus.

FIG._3B

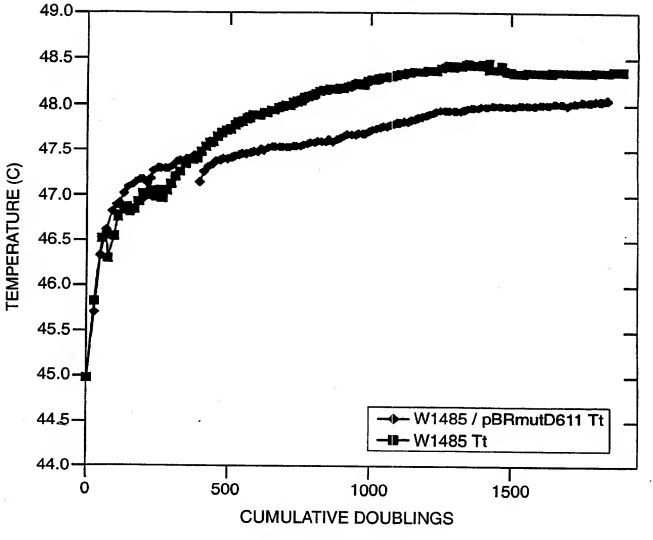

49.0
48.5
48.0
47.5
47.0
46.5
46.0
45.5
45.0
44.5
44.0
TEMPERATURE (C)
0
500
1000
1500
CUMULATIVE DOUBLINGS
W1485 / pBRmutD611 Tt
W1485 Tt

FIG._4

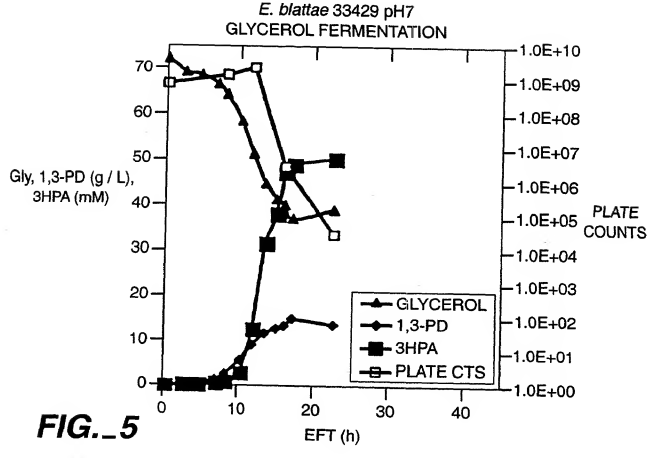

E. blattae 33429 pH7
GLYCEROL FERMENTATION
Gly, 1,3-PD (g / L),
3HPA (mM)
PLATE
COUNTS
GLYCEROL
1,3-PD
3HPA
PLATE CTS
EFT (h)

FIG._5

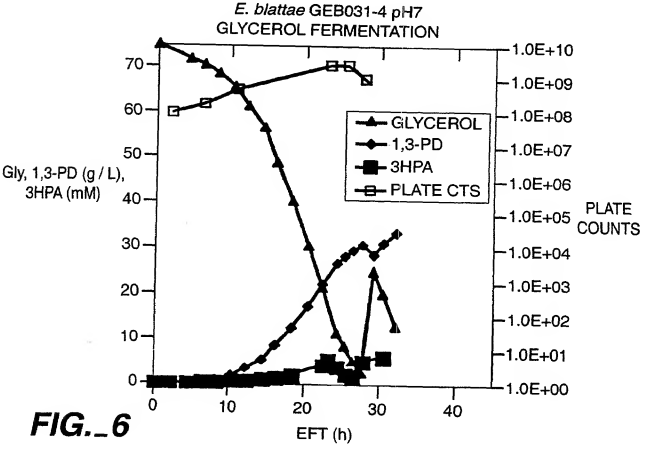

E. blattae GEB031-4 pH7
GLYCEROL FERMENTATION
Gly, 1,3-PD (g / L),
3HPA (mM)
PLATE
COUNTS
GLYCEROL
1,3-PD
3HPA
PLATE CTS
EFT (h)

FIG._6